Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Period: \_\_\_\_\_\_

**Fruit Fly Genetics: Virtual Lab**

Ms. Ottolini, AP Biology, 2012-2013

**Overview:** One of the most popular organisms for genetic studies is the fruit fly *Drosophila melanogaster.* Two traits that make *Drosophila* an excellent model organism are its rapid reproduction rate and easily distinguishable phenotypes. In our virtual lab, we will be studying the inheritance patterns of two traits: eye color and wing size. The "wild type" or normal fruit fly has round red eyes and long, smooth wings. Mutations of these traits are listed below.

***Sepia (eye color)***:  A recessive mutant eye color, with the eyes appearing brownish-red as the individuals emerge from the pupa, and darkening to nearly black in older adults.  Wild-type allele is S and mutant is s.

***Vestigial (wing size)***:  A recessive wing mutation resulting in small, shriveled wings. The wild-type allele is V and the recessive allele is v.

***White (eye color)***:  A sex-linked, recessive mutant eye color, with the eyes appearing white or colorless.  This gene locus is found on the X chromosome. (The Y chromosome which determines maleness does not carry this locus.) The wild-type allele is XW and the mutant allele is Xw.

In this lab, we will be performing crosses between fruit flies with different eye colors and wing sizes to determine observed offspring phenotype ratios. We will then compare these observed ratios with expected ratios from Punnett square analyses we performed before the lab. Our tool for statistical comparison will be a chi-square analysis.

In this lab, we will be performing the three crosses listed in the chart below. For each cross, we will obtain our F1 offspring and re-cross them to obtain our F2 offspring:

|  |  |  |  |
| --- | --- | --- | --- |
| **Cross #** | **Type of Cross** | **Male Fly** | **Female Fly** |
| 1 | Normal Monohybrid | Sepia Eyes | Wild Type Eyes (Red) |
| 2 | Sex-Linked Monohybrid | Wild Type Eyes (Red) | White Eyes |
| 3 | Dihybrid | Sepia Eyes, Normal Wings | Wild Type Eyes (Red), Vestigial Wings |

**Pre-Lab:** Complete each of the crosses using the Punnett Squares given below.

1. Sepia-Eyed Male x Red-Eyed Female

P cross (ss x SS) F1 Cross (\_\_\_\_\_\_\_\_ x \_\_\_\_\_\_\_\_)

|  |  |
| --- | --- |
|  |  |
|  |  |

|  |  |
| --- | --- |
|  |  |
|  |  |

F1 Genotypes: F2 Genotypes:

F1 Phenotypes: F2 Phenotypes:

1. Red-Eyed Male x White-Eyed Female

P cross (XWY x XwXw) F1 Cross (\_\_\_\_\_\_\_\_ x \_\_\_\_\_\_\_\_)

|  |  |
| --- | --- |
|  |  |
|  |  |

F1 Genotypes: F2 Genotypes:

F1 Phenotypes F2 Phenotypes:

1. Sepia-Eyed, Normal-Winged Male x Red-Eyed, Vestigial-Winged Female

P cross (ssVV x SSvv)

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
|  |  |  | F1 Genotypes:  F1 Phenotypes: |
|  |  |  |  |
|  |  |  |  |

F1 Cross (\_\_\_\_\_\_\_\_\_\_\_\_\_ x \_\_\_\_\_\_\_\_\_\_\_\_\_\_)

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
|  |  |  | F2 Genotypes: **TOO COMPLICATED**  F2 Phenotypes: |
|  |  |  |  |
|  |  |  |  |

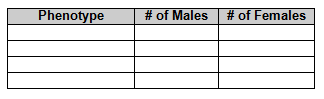
**Lab Instructions**

1. Sign in to your computer using Username: student, Password: student. Check the “Workstation Only” box.
2. Go to the following URL address: <http://www.sciencecourseware.org/vcise/drosophila/>
3. Click the “Enter as a Guest” option.
4. The first thing you must do is order the fruit flies for your first cross. Click on the computer and use the “Order Flies” icon.
5. After ordering your flies, the software will give you instructions on how to cross the flies and sort the F1 offspring by phenotype using a microscope view. Make sure you record the data for your F1 generation in your data table.
6. After you have recorded the data, you will need to establish a cross between members of your F1 generation. To do this, click on the piles of sorted flies to zoom in. Then click the “Use in New Mating” button. Do this for both a male and a female. Then return to your lab. Click on the mating jar and continue with the cross to obtain your F2 generation. Make sure you record the data for your F2 generation in your data table.
7. After you collect F2 data, clean out incubator by clicking on the small trash can next to it. This resets your lab for the next cross.
8. Follow Steps 4-6 for your remaining two crosses.

**Lab Data**

***Table 1:*** Sepia-Eyed Male x Red-Eyed Female (Cross 1)

Phenotypes of the F1 Generation Phenotypes of F2 Generation

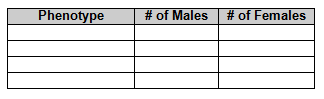


|  |  |  |
| --- | --- | --- |
| **Phenotype** | **# of Males** | **# of Females** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

***Conclusions:*** After “eyeballing” the data, do your observed results seem to match with your expected results? Does it seem that this is an autosomal recessive method of inheritance?

***Table 2:*** Red-Eyed Male x White-Eyed Female (Cross 2)

Phenotypes of the F1 Generation Phenotypes of F2 Generation

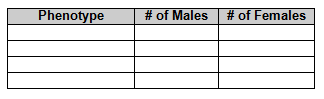
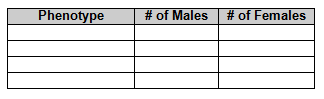


|  |  |  |
| --- | --- | --- |
| **Phenotype** | **# of Males** | **# of Females** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

***Conclusions:*** After “eyeballing” the data, do your observed results seem to match with your expected results? Does it seem that this is a sex-linked recessive method of inheritance?

***Table 3:*** Sepia-Eyed, Normal-Winged Male x Red-Eyed, Vestigial-Winged Female (Cross 3)

Phenotypes of the F1 Generation Phenotypes of F2 Generation



|  |  |  |
| --- | --- | --- |
| **Phenotype** | **# of Males** | **# of Females** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

***Conclusions:*** After “eyeballing” the data, do your observed results seem to match with your expected results? Does it seem that both of these traits are inherited as autosomal recessive traits?

**Post-Lab:** Chi square analysis of F2 offspring from Cross #1.

1. How many total offspring (males + females) were in the F2 generation from our first cross?
2. Calculate your expected #’s of flies with each phenotype using the following formula: % expected x total #.

|  |  |  |
| --- | --- | --- |
| **Phenotype** | **% Expected**  **(expressed as a decimal)** | **# of flies expected:**  **% expected x total # of flies** |
| Red Eyes |  |  |
| Sepia Eyes |  |  |

Use the table below to determine your X2 value for your data.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phenotype** | **# Observed (o)** | **# Expected (e)** | **(o-e)** | **(o-e)2** | **(o-e)2 / e** |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

Total (add the values in the last column) = **X2 value** = \_\_\_\_\_\_\_\_\_

1. How many degrees of freedom should we use? Remember, the degrees of freedom represent the number of classes of data minus one.
2. Use the chart below to determine the p value (probability) from your X2 value and degrees of freedom. Make an estimate of the p value if your X2 value is somewhere in between the given values.



**P value = \_\_\_\_\_\_\_\_\_\_\_**

1. Based on your p value, do you accept or reject your null hypothesis (the expected phenotypes for the F2 offspring)? *Remember, a p value below 0.05 indicates that there were significant differences between the observed and expected results that cannot be explained by chance. If you have a p value below 0.05 you must reject your null hypothesis. A p value above 0.05 indicates that the observed and expected results were very close, and any differences can be explained by random chance. If you have a p value above 0.05 you must accept your null hypothesis.*